

SEQUENCE LISTING

<110> Sprecher, Cindy A.
 Novak, Julia E.
 West, James W.
 Presnell, Scott R.
 Holly, Richard D.
 Nelson, Andrew J.

<120> SOLUBLE ZALPHA11 CYTOKINE RECEPTORS

<130> 00-22

<150> US 60/194,731

<151> 2000-04-05

<150> US 60/222,121

<151> 2000-07-28

<160> 86

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1614

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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1				5				10						15		

ggc	tgg	ggc	tgc	ccc	gac	ctc	gtc	tgc	tac	acc	gat	tac	ctc	cag	acg	96
Gly	Trp	Gly	Cys	Pro	Asp	Leu	Val	Cys	Tyr	Thr	Asp	Tyr	Leu	Gln	Thr	
			20					25						30		

gtc	atc	tgc	atc	ctg	gaa	atg	tgg	aac	ctc	cac	ccc	agc	acg	ctc	acc	144
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Val	Ile	Cys	Ile	Leu	Glu	Met	Trp	Asn	Leu	His	Pro	Ser	Thr	Leu	Thr		
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ctt	acc	tgg	caa	gac	cag	tat	gaa	gag	ctg	aag	gac	gag	gcc	acc	tcc		192
Leu	Thr	Trp	Gln	Asp	Gln	Tyr	Glu	Glu	Leu	Lys	Asp	Glu	Ala	Thr	Ser		
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Cys	Ser	Leu	His	Arg	Ser	Ala	His	Asn	Ala	Thr	His	Ala	Thr	Tyr	Thr		
	65				70				75						80		
tgc	cac	atg	gat	gta	ttc	cac	ttc	atg	gcc	gac	gac	att	ttc	agt	gtc		288
Cys	His	Met	Asp	Val	Phe	His	Phe	Met	Ala	Asp	Asp	Ile	Phe	Ser	Val		
				85					90					95			
aac	atc	aca	gac	cag	tct	ggc	aac	tac	tcc	cag	gag	tgt	ggc	agc	ttt		336
Asn	Ile	Thr	Asp	Gln	Ser	Gly	Asn	Tyr	Ser	Gln	Glu	Cys	Gly	Ser	Phe		
			100					105					110				
ctc	ctg	gct	gag	agc	atc	aag	ccg	gct	ccc	cct	ttc	aac	gtg	act	gtg		384
Leu	Leu	Ala	Glu	Ser	Ile	Lys	Pro	Ala	Pro	Pro	Phe	Asn	Val	Thr	Val		
		115					120					125					
acc	ttc	tca	gga	cag	tat	aat	atc	tcc	tgg	cgc	tca	gat	tac	gaa	gac		432
Thr	Phe	Ser	Gly	Gln	Tyr	Asn	Ile	Ser	Trp	Arg	Ser	Asp	Tyr	Glu	Asp		
	130					135					140						
cct	gcc	ttc	tac	atg	ctg	aag	ggc	aag	ctt	cag	tat	gag	ctg	cag	tac		480
Pro	Ala	Phe	Tyr	Met	Leu	Lys	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln	Tyr		
	145				150				155					160			
agg	aac	cgg	gga	gac	ccc	tgg	gct	gtg	agt	ccg	agg	aga	aag	ctg	atc		528
Arg	Asn	Arg	Gly	Asp	Pro	Trp	Ala	Val	Ser	Pro	Arg	Arg	Lys	Leu	Ile		
				165					170					175			
tca	gtg	gac	tca	aga	agt	gtc	tcc	ctc	ctc	ccc	ctg	gag	ttc	cgc	aaa		576
Ser	Val	Asp	Ser	Arg	Ser	Val	Ser	Leu	Leu	Pro	Leu	Glu	Phe	Arg	Lys		
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gac	tcg	agc	tat	gag	ctg	cag	gtg	cgg	gca	ggg	ccc	atg	cct	ggc	tcc		624
Asp	Ser	Ser	Tyr	Glu	Leu	Gln	Val	Arg	Ala	Gly	Pro	Met	Pro	Gly	Ser		
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acc cag tca gag gag tta aag gaa ggc tgg aac cct cac ctg ctg ctt Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu 225 230 235 240	720
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acc cat cca ttg tgg agg cta tgg aag aag ata tgg gcc gtc ccc agc Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser 260 265 270	816
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cca cca cgg agc ccg gcc aag agg ctg cag ctc acg gag cta caa gaa Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu 325 330 335	1008
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Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro	
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gcc ctg gac ctg gat gct ggc ctg gag ccc agc cca ggc cta gag gac	1248
Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp	
405 410 415	
cca ctc ttg gat gca ggg acc aca gtc ctg tcc tgt ggc tgt gtc tca	1296
Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser	
420 425 430	
gct ggc agc cct ggg cta gga ggg ccc ctg gga agc ctc ctg gac aga	1344
Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg	
435 440 445	
cta aag cca ccc ctt gca gat ggg gag gac tgg gct ggg gga ctg ccc	1392
Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro	
450 455 460	
tgg ggt ggc cgg tca cct gga ggg gtc tca gag agt gag gcg ggc tca	1440
Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser	
465 470 475 480	
ccc ctg gcc ggc ctg gat atg gac acg ttt gac agt ggc ttt gtg ggc	1488
Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly	
485 490 495	
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Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp	
500 505 510	
gaa gga ccc ccc cgg agc tac ctc cgc cag tgg gtg gtc att cct ccg	1584
Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro	
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<211> 538

<212> PRT

<213> Homo sapiens

<400> 2

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Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr
 35          40          45
Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
 50          55          60
Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
 65          70          75          80
Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
 85          90          95
Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe
100          105          110
Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val
115          120          125
Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp
130          135          140
Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
145          150          155          160
Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile
165          170          175
Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys
180          185          190
Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser
195          200          205
Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
210          215          220
Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu
225          230          235          240
Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys
245          250          255
Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser
260          265          270
Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe
275          280          285
Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly
290          295          300

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Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His
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 Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu
 325 330 335
 Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp
 340 345 350
 Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp
 355 360 365
 Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala
 370 375 380
 Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro
 385 390 395 400
 Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp
 405 410 415
 Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser
 420 425 430
 Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg
 435 440 445
 Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro
 450 455 460
 Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser
 465 470 475 480
 Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly
 485 490 495
 Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp
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 Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser
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 <213> Homo sapiens

<220>
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gat	ttc	ttc	ctg	acc	act	atg	ccc	act	gac	tcc	ctc	agt	gtt	tcc	act	96
Asp	Phe	Phe	Leu	Thr	Thr	Met	Pro	Thr	Asp	Ser	Leu	Ser	Val	Ser	Thr	
			20					25					30			
ctg	ccc	ctc	cca	gag	gtt	cag	tgt	ttt	gtg	ttc	aat	gtc	gag	tac	atg	144
Leu	Pro	Leu	Pro	Glu	Val	Gln	Cys	Phe	Val	Phe	Asn	Val	Glu	Tyr	Met	
			35				40					45				
aat	tgc	act	tgg	aac	agc	agc	tct	gag	ccc	cag	cct	acc	aac	ctc	act	192
Asn	Cys	Thr	Trp	Asn	Ser	Ser	Ser	Glu	Pro	Gln	Pro	Thr	Asn	Leu	Thr	
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ctg	cat	tat	tgg	tac	aag	aac	tcg	gat	aat	gat	aaa	gtc	cag	aag	tgc	240
Leu	His	Tyr	Trp	Tyr	Lys	Asn	Ser	Asp	Asn	Asp	Lys	Val	Gln	Lys	Cys	
	65				70				75						80	
agc	cac	tat	cta	ttc	tct	gaa	gaa	atc	act	tct	ggc	tgt	cag	ttg	caa	288
Ser	His	Tyr	Leu	Phe	Ser	Glu	Glu	Ile	Thr	Ser	Gly	Cys	Gln	Leu	Gln	
				85				90						95		
aaa	aag	gag	atc	cac	ctc	tac	caa	aca	ttt	gtt	gtt	cag	ctc	cag	gac	336
Lys	Lys	Glu	Ile	His	Leu	Tyr	Gln	Thr	Phe	Val	Val	Gln	Leu	Gln	Asp	
			100					105					110			
cca	cgg	gaa	ccc	agg	aga	cag	gcc	aca	cag	atg	cta	aaa	ctg	cag	aat	384
Pro	Arg	Glu	Pro	Arg	Arg	Gln	Ala	Thr	Gln	Met	Leu	Lys	Leu	Gln	Asn	
			115				120					125				
ctg	gtg	atc	ccc	tgg	gct	cca	gag	aac	cta	aca	ctt	cac	aaa	ctg	agt	432
Leu	Val	Ile	Pro	Trp	Ala	Pro	Glu	Asn	Leu	Thr	Leu	His	Lys	Leu	Ser	
	130					135					140					
gaa	tcc	cag	cta	gaa	ctg	aac	tgg	aac	aac	aga	ttc	ttg	aac	cac	tgt	480
Glu	Ser	Gln	Leu	Glu	Leu	Asn	Trp	Asn	Asn	Arg	Phe	Leu	Asn	His	Cys	
	145				150				155						160	
ttg	gag	cac	ttg	gtg	cag	tac	cgg	act	gac	tgg	gac	cac	agc	tgg	act	528
Leu	Glu	His	Leu	Val	Gln	Tyr	Arg	Thr	Asp	Trp	Asp	His	Ser	Trp	Thr	
				165				170						175		

gaa caa tca gtg gat tat aga cat aag ttc tcc ttg cct agt gtg gat 576
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 180 185 190

ggg cag aaa cgc tac acg ttt cgt gtt cgg agc cgc ttt aac cca ctc 624
 Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg Ser Arg Phe Asn Pro Leu
 195 200 205

tgt gga agt gct cag cat tgg agt gaa tgg agc cac cca atc cac tgg 672
 Cys Gly Ser Ala Gln His Trp Ser Glu Trp Ser His Pro Ile His Trp
 210 215 220

ggg agc aat act tca aaa gag aat 696
 Gly Ser Asn Thr Ser Lys Glu Asn
 225 230

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 <213> Homo sapiens

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 35 40 45
 Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro Gln Pro Thr Asn Leu Thr
 50 55 60
 Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn Asp Lys Val Gln Lys Cys
 65 70 75 80
 Ser His Tyr Leu Phe Ser Glu Glu Ile Thr Ser Gly Cys Gln Leu Gln
 85 90 95
 Lys Lys Glu Ile His Leu Tyr Gln Thr Phe Val Val Gln Leu Gln Asp
 100 105 110
 Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln Met Leu Lys Leu Gln Asn
 115 120 125
 Leu Val Ile Pro Trp Ala Pro Glu Asn Leu Thr Leu His Lys Leu Ser
 130 135 140
 Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn Arg Phe Leu Asn His Cys
 145 150 155 160

Leu Glu His Leu Val Gln Tyr Arg Thr Asp Trp Asp His Ser Trp Thr
 165 170 175
 Glu Gln Ser Val Asp Tyr Arg His Lys Phe Ser Leu Pro Ser Val Asp
 180 185 190
 Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg Ser Arg Phe Asn Pro Leu
 195 200 205
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 Gly Ser Asn Thr Ser Lys Glu Asn
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 Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr Leu Thr Trp
 20 25 30

caa gac cag tat gaa gag ctg aag gac gag gcc acc tcc tgc agc ctc 144
 Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu
 35 40 45

cac agg tcg gcc cac aat gcc acg cat gcc acc tac acc tgc cac atg 192
 His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr Cys His Met
 50 55 60

gat gta ttc cac ttc atg gcc gac gac att ttc agt gtc aac atc aca 240
 Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr
 65 70 75 80

gac cag tct ggc aac tac tcc cag gag tgt ggc agc ttt ctc ctg gct 288

Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala
 85 90 95

gag agc atc aag ccg gct ccc cct ttc aac gtg act gtg acc ttc tca 336
 Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val Thr Phe Ser
 100 105 110

gga cag tat aat atc tcc tgg cgc tca gat tac gaa gac cct gcc ttc 384
 Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe
 115 120 125

tac atg ctg aag ggc aag ctt cag tat gag ctg cag tac agg aac cgg 432
 Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg
 130 135 140

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 Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp
 145 150 155 160

tca aga agt gtc tcc ctc ctc ccc ctg gag ttc cgc aaa gac tcg agc 528
 Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser
 165 170 175

tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc tcc tcc tac cag 576
 Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln
 180 185 190

ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt cag acc cag tca 624
 Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser
 195 200 205

gag gag tta aag gaa ggc tgg aac cct cac 654
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 210 215

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<212> PRT

<213> Homo sapiens

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 Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu
 35 40 45
 His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr Cys His Met
 50 55 60
 Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr
 65 70 75 80
 Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala
 85 90 95
 Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val Thr Phe Ser
 100 105 110
 Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe
 115 120 125
 Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg
 130 135 140
 Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp
 145 150 155 160
 Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser
 165 170 175
 Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln
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 Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser
 195 200 205
 Glu Glu Leu Lys Glu Gly Trp Asn Pro His
 210 215

<210> 7
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate polynucleotide sequence of soluble
 zalpha11 Receptor polypeptide as shown in SEQ ID
 NO:6

<221> misc_feature
 <222> (1)...(654)
 <223> n = A,T,C or G

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gaygargcna cnwsntgyws nytncaymgn wsnencaya aygcnacnca ygcnaentay	180
acntgycaya tggaygtntt ycayttyatg gcngaygaya thttywsngt naayathacn	240
gaycarwsng gnaaytayws ncargartgy ggnwsnttyy tnytngcnga rwsnathaar	300
ccngcncnc cnttyaaygt nacngtnacn ttywsnggnc artayaayat hwsntggmgn	360
wsngaytayg argayccngc nttytayatg ytnaarggna arytncarta ygarytncar	420
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wsnmgnwsng tnwsnytnyt nccnytngar ttymгнаarg aywsnwsnta ygarytncar	540
gtmngngcng gncnatgcc nggnwsnwsn taycarggna cntggwsnga rtggwsngay	600
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<212> DNA

<213> Artificial Sequence

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<223> Degenerate polynucleotide sequence of IL-2Rgamma
polypeptide as shown in SEQ ID NO:4

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<222> (1)...(696)

<223> n = A,T,C or G

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ttygtnttya aygtngarta yatgaaytgy acntggaayw snwsnwsnga rccncarccn	180
acnaayytna cnytncayta ytggtayaar aaywsngaya aygayaargt ncaraartgy	240
wsncaytayy tnttywsnga rgarathacn wsnngntgyc arytncaraa raargarath	300
cayytnayc aracnttygt ngtncarytn cargayccnm gngarccnmg nmgnargcn	360
acncaratgy tnaarytnca raayytngtn athccntggg cncngaraa yytnacnytn	420
cayaarytnw sngarwsnca rytngarytn aaytggaaya aymgnttyt naaycaytgy	480
ytnargcayy tngtncarta ymgnacngay tgggaycayw sntggacnga rcarwsngtn	540
gaytaymgnc ayaarttyws nytnccnwsn gtngayggnc araarmgnta yacnttymgn	600
gtmgnwsnm gnttyaaycc nytntygggn wsnencarc aytggwsnga rtggwsncay	660
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<212> DNA
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1 5 10 15	
gtc atc ttc ttg ggg aca ctg gtc cac aaa tca agc tcc caa ggt caa	96
Val Ile Phe Leu Gly Thr Leu Val His Lys Ser Ser Ser Gln Gly Gln	
20 25 30	
gat cgc cac atg att aga atg cgt caa ctt ata gat att gtt gat cag	144
Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp Ile Val Asp Gln	
35 40 45	
ctg aaa aat tat gtg aat gac ttg gtc cct gaa ttt ctg cca gct cca	192
Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu Pro Ala Pro	
50 55 60	
gaa gat gta gag aca aac tgt gag tgg tca gct ttt tcc tgt ttt cag	240
Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser Cys Phe Gln	
65 70 75 80	
aag gcc caa cta aag tca gca aat aca gga aac aat gaa agg ata atc	288
Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu Arg Ile Ile	
85 90 95	
aat gta tca att aaa aag ctg aag agg aaa cca cct tcc aca aat gca	336
Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser Thr Asn Ala	
100 105 110	
ggg aga aga cag aaa cac aga cta aca tgc cct tca tgt gat tct tat	384
Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys Asp Ser Tyr	
115 120 125	
gag aaa aaa cca ccc aaa gaa ttc cta gaa aga ttc aaa tca ctt ctc	432
Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys Ser Leu Leu	
130 135 140	

caa aag atg att cat cag cat ctg tcc tct aga aca cac gga agt gaa 480
 Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr His Gly Ser Glu
 145 150 155 160

gat tcc 486
 Asp Ser

<210> 10
 <211> 162
 <212> PRT
 <213> Homo sapiens

<400> 10
 Met Arg Ser Ser Pro Gly Asn Met Glu Arg Ile Val Ile Cys Leu Met
 1 5 10 15
 Val Ile Phe Leu Gly Thr Leu Val His Lys Ser Ser Ser Gln Gly Gln
 20 25 30
 Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp Ile Val Asp Gln
 35 40 45
 Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu Pro Ala Pro
 50 55 60
 Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser Cys Phe Gln
 65 70 75 80
 Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu Arg Ile Ile
 85 90 95
 Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser Thr Asn Ala
 100 105 110
 Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys Asp Ser Tyr
 115 120 125
 Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys Ser Leu Leu
 130 135 140
 Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr His Gly Ser Glu
 145 150 155 160
 Asp Ser

<210> 11
 <211> 1735
 <212> DNA
 <213> mus musculus

<220>
 <221> CDS

<222> (143)...(1729)

<400> 11

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cgcccaggag accaccaag tgcccagcc taaagaatgg ctttctgaga aagaccctga	120
aggagtaggt ctgggacaca gc atg ccc cgg ggc cca gtg gct gcc tta ctc	172
Met Pro Arg Gly Pro Val Ala Ala Leu Leu	
1 5 10	
ctg ctg att ctc cat gga gct tgg agc tgc ctg gac ctc act tgc tac	220
Leu Leu Ile Leu His Gly Ala Trp Ser Cys Leu Asp Leu Thr Cys Tyr	
15 20 25	
act gac tac ctc tgg acc atc acc tgt gtc ctg gag aca cgg agc ccc	268
Thr Asp Tyr Leu Trp Thr Ile Thr Cys Val Leu Glu Thr Arg Ser Pro	
30 35 40	
aac ccc agc ata ctc agt ctc acc tgg caa gat gaa tat gag gaa ctt	316
Asn Pro Ser Ile Leu Ser Leu Thr Trp Gln Asp Glu Tyr Glu Glu Leu	
45 50 55	
cag gac caa gag acc ttc tgc agc cta cac agg tct ggc cac aac acc	364
Gln Asp Gln Glu Thr Phe Cys Ser Leu His Arg Ser Gly His Asn Thr	
60 65 70	
aca cat ata tgg tac acg tgc cat atg cgc ttg tct caa ttc ctg tcc	412
Thr His Ile Trp Tyr Thr Cys His Met Arg Leu Ser Gln Phe Leu Ser	
75 80 85 90	
gat gaa gtt ttc att gtc aat gtg acg gac cag tct ggc aac aac tcc	460
Asp Glu Val Phe Ile Val Asn Val Thr Asp Gln Ser Gly Asn Asn Ser	
95 100 105	
caa gag tgt ggc agc ttt gtc ctg gct gag agc atc aaa cca gct ccc	508
Gln Glu Cys Gly Ser Phe Val Leu Ala Glu Ser Ile Lys Pro Ala Pro	
110 115 120	
ccc ttg aac gtg act gtg gcc ttc tca gga cgc tat gat atc tcc tgg	556
Pro Leu Asn Val Thr Val Ala Phe Ser Gly Arg Tyr Asp Ile Ser Trp	
125 130 135	
gac tca gct tat gac gaa ccc tcc aac tac gtg ctg agg ggc aag cta	604

Asp Ser Ala Tyr Asp Glu Pro Ser Asn Tyr Val Leu Arg Gly Lys Leu	
140 145 150	
caa tat gag ctg cag tat cgg aac ctc aga gac ccc tat gct gtg agg	652
Gln Tyr Glu Leu Gln Tyr Arg Asn Leu Arg Asp Pro Tyr Ala Val Arg	
155 160 165 170	
ccg gtg acc aag ctg atc tca gtg gac tca aga aac gtc tct ctt ctc	700
Pro Val Thr Lys Leu Ile Ser Val Asp Ser Arg Asn Val Ser Leu Leu	
175 180 185	
cct gaa gag ttc cac aaa gat tct agc tac cag ctg cag gtg cgg gca	748
Pro Glu Glu Phe His Lys Asp Ser Ser Tyr Gln Leu Gln Val Arg Ala	
190 195 200	
gcg cct cag cca ggc act tca ttc agg ggg acc tgg agt gag tgg agt	796
Ala Pro Gln Pro Gly Thr Ser Phe Arg Gly Thr Trp Ser Glu Trp Ser	
205 210 215	
gac ccc gtc atc ttt cag acc cag gct ggg gag ccc gag gca ggc tgg	844
Asp Pro Val Ile Phe Gln Thr Gln Ala Gly Glu Pro Glu Ala Gly Trp	
220 225 230	
gac cct cac atg ctg ctg ctc ctg gct gtc ttg atc att gtc ctg gtt	892
Asp Pro His Met Leu Leu Leu Leu Ala Val Leu Ile Ile Val Leu Val	
235 240 245 250	
ttc atg ggt ctg aag atc cac ctg cct tgg agg cta tgg aaa aag ata	940
Phe Met Gly Leu Lys Ile His Leu Pro Trp Arg Leu Trp Lys Lys Ile	
255 260 265	
tgg gca cca gtg ccc acc cct gag agt ttc ttc cag ccc ctg tac agg	988
Trp Ala Pro Val Pro Thr Pro Glu Ser Phe Phe Gln Pro Leu Tyr Arg	
270 275 280	
gag cac agc ggg aac ttc aag aaa tgg gtt aat acc cct ttc acg gcc	1036
Glu His Ser Gly Asn Phe Lys Lys Trp Val Asn Thr Pro Phe Thr Ala	
285 290 295	
tcc agc ata gag ttg gtg cca cag agt tcc aca aca aca tca gcc tta	1084
Ser Ser Ile Glu Leu Val Pro Gln Ser Ser Thr Thr Thr Ser Ala Leu	
300 305 310	

cat ctg tca ttg tat cca gcc aag gag aag aag ttc ccg ggg ctg ccg	1132
His Leu Ser Leu Tyr Pro Ala Lys Glu Lys Lys Phe Pro Gly Leu Pro	
315 320 325 330	
ggt ctg gaa gag caa ctg gag tgt gat gga atg tct gag cct ggt cac	1180
Gly Leu Glu Glu Gln Leu Glu Cys Asp Gly Met Ser Glu Pro Gly His	
335 340 345	
tgg tgc ata atc ccc ttg gca gct ggc caa gcg gtc tca gcc tac agt	1228
Trp Cys Ile Ile Pro Leu Ala Ala Gly Gln Ala Val Ser Ala Tyr Ser	
350 355 360	
gag gag aga gac cgg cca tat ggt ctg gtg tcc att gac aca gtg act	1276
Glu Glu Arg Asp Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr	
365 370 375	
gtg gga gat gca gag ggc ctg tgt gtc tgg ccc tgt agc tgt gag gat	1324
Val Gly Asp Ala Glu Gly Leu Cys Val Trp Pro Cys Ser Cys Glu Asp	
380 385 390	
gat ggc tat cca gcc atg aac ctg gat gct ggc cga gag tct ggc cct	1372
Asp Gly Tyr Pro Ala Met Asn Leu Asp Ala Gly Arg Glu Ser Gly Pro	
395 400 405 410	
aat tca gag gat ctg ctc ttg gtc aca gac cct gct ttt ctg tct tgc	1420
Asn Ser Glu Asp Leu Leu Leu Val Thr Asp Pro Ala Phe Leu Ser Cys	
415 420 425	
ggc tgt gtc tca ggt agt ggt ctc agg ctt gga ggc tcc cca ggc agc	1468
Gly Cys Val Ser Gly Ser Gly Leu Arg Leu Gly Gly Ser Pro Gly Ser	
430 435 440	
cta ctg gac agg ttg agg ctg tca ttt gca aag gaa ggg gac tgg aca	1516
Leu Leu Asp Arg Leu Arg Leu Ser Phe Ala Lys Glu Gly Asp Trp Thr	
445 450 455	
gca gac cca acc tgg aga act ggg tcc cca gga ggg ggc tct gag agt	1564
Ala Asp Pro Thr Trp Arg Thr Gly Ser Pro Gly Gly Gly Ser Glu Ser	
460 465 470	
gaa gca ggt tcc ccc cct ggt ctg gac atg gac aca ttt gac agt ggc	1612

Glu Ala Gly Ser Pro Pro Gly Leu Asp Met Asp Thr Phe Asp Ser Gly
475 480 485 490

ttt gca ggt tca gac tgt ggc agc ccc gtg gag act gat gaa gga ccc 1660
Phe Ala Gly Ser Asp Cys Gly Ser Pro Val Glu Thr Asp Glu Gly Pro
495 500 505

cct cga agc tat ctc cgc cag tgg gtg gtc agg acc cct cca cct gtg 1708
Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Arg Thr Pro Pro Pro Val
510 515 520

gac agt gga gcc cag agc agc tagcat 1735
Asp Ser Gly Ala Gln Ser Ser
525

<210> 12

<211> 529

<212> PRT

<213> mus musculus

<400> 12

Met Pro Arg Gly Pro Val Ala Ala Leu Leu Leu Ile Leu His Gly
1 5 10 15
Ala Trp Ser Cys Leu Asp Leu Thr Cys Tyr Thr Asp Tyr Leu Trp Thr
20 25 30
Ile Thr Cys Val Leu Glu Thr Arg Ser Pro Asn Pro Ser Ile Leu Ser
35 40 45
Leu Thr Trp Gln Asp Glu Tyr Glu Glu Leu Gln Asp Gln Glu Thr Phe
50 55 60
Cys Ser Leu His Arg Ser Gly His Asn Thr Thr His Ile Trp Tyr Thr
65 70 75 80
Cys His Met Arg Leu Ser Gln Phe Leu Ser Asp Glu Val Phe Ile Val
85 90 95
Asn Val Thr Asp Gln Ser Gly Asn Asn Ser Gln Glu Cys Gly Ser Phe
100 105 110
Val Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Leu Asn Val Thr Val
115 120 125
Ala Phe Ser Gly Arg Tyr Asp Ile Ser Trp Asp Ser Ala Tyr Asp Glu
130 135 140
Pro Ser Asn Tyr Val Leu Arg Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
145 150 155 160

Arg Asn Leu Arg Asp Pro Tyr Ala Val Arg Pro Val Thr Lys Leu Ile
 165 170 175
 Ser Val Asp Ser Arg Asn Val Ser Leu Leu Pro Glu Glu Phe His Lys
 180 185 190
 Asp Ser Ser Tyr Gln Leu Gln Val Arg Ala Ala Pro Gln Pro Gly Thr
 195 200 205
 Ser Phe Arg Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
 210 215 220
 Thr Gln Ala Gly Glu Pro Glu Ala Gly Trp Asp Pro His Met Leu Leu
 225 230 235 240
 Leu Leu Ala Val Leu Ile Ile Val Leu Val Phe Met Gly Leu Lys Ile
 245 250 255
 His Leu Pro Trp Arg Leu Trp Lys Lys Ile Trp Ala Pro Val Pro Thr
 260 265 270
 Pro Glu Ser Phe Phe Gln Pro Leu Tyr Arg Glu His Ser Gly Asn Phe
 275 280 285
 Lys Lys Trp Val Asn Thr Pro Phe Thr Ala Ser Ser Ile Glu Leu Val
 290 295 300
 Pro Gln Ser Ser Thr Thr Thr Ser Ala Leu His Leu Ser Leu Tyr Pro
 305 310 315 320
 Ala Lys Glu Lys Lys Phe Pro Gly Leu Pro Gly Leu Glu Glu Gln Leu
 325 330 335
 Glu Cys Asp Gly Met Ser Glu Pro Gly His Trp Cys Ile Ile Pro Leu
 340 345 350
 Ala Ala Gly Gln Ala Val Ser Ala Tyr Ser Glu Glu Arg Asp Arg Pro
 355 360 365
 Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Gly Asp Ala Glu Gly
 370 375 380
 Leu Cys Val Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro Ala Met
 385 390 395 400
 Asn Leu Asp Ala Gly Arg Glu Ser Gly Pro Asn Ser Glu Asp Leu Leu
 405 410 415
 Leu Val Thr Asp Pro Ala Phe Leu Ser Cys Gly Cys Val Ser Gly Ser
 420 425 430
 Gly Leu Arg Leu Gly Gly Ser Pro Gly Ser Leu Leu Asp Arg Leu Arg
 435 440 445
 Leu Ser Phe Ala Lys Glu Gly Asp Trp Thr Ala Asp Pro Thr Trp Arg
 450 455 460
 Thr Gly Ser Pro Gly Gly Gly Ser Glu Ser Glu Ala Gly Ser Pro Pro
 465 470 475 480
 Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Ala Gly Ser Asp Cys
 485 490 495

Gly Ser Pro Val Glu Thr Asp Glu Gly Pro Pro Arg Ser Tyr Leu Arg
 500 505 510
 Gln Trp Val Val Arg Thr Pro Pro Pro Val Asp Ser Gly Ala Gln Ser
 515 520 525
 Ser

<210> 13
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> WSXWS polypeptide consensus motif

<221> VARIANT
 <222> (1)...(5)
 <223> Xaa = Any Amino Acid

<400> 13
 Trp Ser Xaa Trp Ser
 1 5

<210> 14
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Glu-Glu (CEE) Tag amino acid sequence

<400> 14
 Glu Tyr Met Pro Met Glu
 1 5

<210> 15
 <211> 1701
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> soluble zalpha11R/IgGgamma1 construct

<221> CDS

<222> (1)...(1701)

<400> 15
 atg ccg cgt ggc tgg gcc gcc ccc ttg ctc ctg ctg ctg ctc cag gga 48
 Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Gln Gly
 1 5 10 15

 ggc tgg ggc tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag acg 96
 Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr
 20 25 30

 gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc acc 144
 Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr
 35 40 45

 ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc tcc 192
 Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
 50 55 60

 tgc agc ctc cac agg tgc gcc cac aat gcc acg cat gcc acc tac acc 240
 Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
 65 70 75 80

 tgc cac atg gat gta ttc cac ttc atg gcc gac gac att ttc agt gtc 288
 Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
 85 90 95

 aac atc aca gac cag tct ggc aac tac tcc cag gag tgt ggc agc ttt 336
 Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe
 100 105 110

 ctc ctg gct gag agc atc aag ccg gct ccc cct ttc aac gtg act gtg 384
 Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val
 115 120 125

 acc ttc tca gga cag tat aat atc tcc tgg cgc tca gat tac gaa gac 432
 Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp
 130 135 140

 cct gcc ttc tac atg ctg aag ggc aag ctt cag tat gag ctg cag tac 480
 Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
 145 150 155 160

agg aac cgg gga gac ccc tgg gct gtg agt ccg agg aga aag ctg atc 528
 Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile
 165 170 175

tca gtg gac tca aga agt gtc tcc ctc ctc ccc ctg gag ttc cgc aaa 576
 Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys
 180 185 190

gac tcg agc tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc tcc 624
 Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser
 195 200 205

tcc tac cag ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt cag 672
 Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
 210 215 220

acc cag tca gag gag tta aag gaa ggc tgg aac cct cac gct agc acc 720
 Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Ala Ser Thr
 225 230 235 240

aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct 768
 Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
 245 250 255

ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa 816
 Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
 260 265 270

ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac 864
 Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
 275 280 285

acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc 912
 Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
 290 295 300

gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc 960
 Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
 305 310 315 320

aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aaa gtt gag 1008

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu	
325 330 335	
ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct	1056
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro	
340 345 350	
gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag	1104
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys	
355 360 365	
gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg	1152
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val	
370 375 380	
gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac	1200
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp	
385 390 395 400	
ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac	1248
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr	
405 410 415	
aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac	1296
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp	
420 425 430	
tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc	1344
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu	
435 440 445	
cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga	1392
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg	
450 455 460	
gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag	1440
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys	
465 470 475 480	
aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac	1488
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp	
485 490 495	

atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag 1536
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 500 505 510

acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc 1584
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 515 520 525

aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca 1632
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 530 535 540

tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc 1680
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 545 550 555 560

ctc tcc ctg tct ccg ggt aaa 1701
 Leu Ser Leu Ser Pro Gly Lys
 565

<210> 16

<211> 567

<212> PRT

<213> Artificial Sequence

<400> 16

Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Gln Gly
 1 5 10 15
 Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr
 20 25 30
 Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr
 35 40 45
 Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
 50 55 60
 Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
 65 70 75 80
 Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
 85 90 95
 Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe
 100 105 110
 Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val
 115 120 125

Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp
 130 135 140
 Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
 145 150 155 160
 Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile
 165 170 175
 Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys
 180 185 190
 Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser
 195 200 205
 Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
 210 215 220
 Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Ala Ser Thr
 225 230 235 240
 Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
 245 250 255
 Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
 260 265 270
 Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
 275 280 285
 Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
 290 295 300
 Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
 305 310 315 320
 Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
 325 330 335
 Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 340 345 350
 Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 355 360 365
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 370 375 380
 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 385 390 395 400
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 405 410 415
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 420 425 430
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 435 440 445
 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 450 455 460

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
 465 470 475 480
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 485 490 495
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 500 505 510
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 515 520 525
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 530 535 540
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 545 550 555 560
 Leu Ser Leu Ser Pro Gly Lys
 565

<210> 17

<211> 1083

<212> DNA

<213> Artificial Sequence

<220>

<223> soluble human IL-2Rgamma/human kappa light chain construct

<221> CDS

<222> (1)...(1083)

<400> 17

atg ttg aag cca tca tta cca ttc aca tcc ctc tta ttc ctg cag ctg 48

Met Leu Lys Pro Ser Leu Pro Phe Thr Ser Leu Leu Phe Leu Gln Leu

1 5 10 15

ccc ctg ctg gga gtg ggg ctg aac acg aca att ctg acg ccc aat ggg 96

Pro Leu Leu Gly Val Gly Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly

20 25 30

aat gaa gac acc aca gct gat ttc ttc ctg acc act atg ccc act gac 144

Asn Glu Asp Thr Thr Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp

35 40 45

tcc ctc agt gtt tcc act ctg ccc ctc cca gag gtt cag tgt ttt gtg 192

Ser	Leu	Ser	Val	Ser	Thr	Leu	Pro	Leu	Pro	Glu	Val	Gln	Cys	Phe	Val		
50						55					60						
ttc	aat	gtc	gag	tac	atg	aat	tgc	act	tgg	aac	agc	agc	tct	gag	ccc	240	
Phe	Asn	Val	Glu	Tyr	Met	Asn	Cys	Thr	Trp	Asn	Ser	Ser	Ser	Glu	Pro		
65					70				75					80			
cag	cct	acc	aac	ctc	act	ctg	cat	tat	tgg	tac	aag	aac	tcg	gat	aat	288	
Gln	Pro	Thr	Asn	Leu	Thr	Leu	His	Tyr	Trp	Tyr	Lys	Asn	Ser	Asp	Asn		
			85					90						95			
gat	aaa	gtc	cag	aag	tgc	agc	cac	tat	cta	ttc	tct	gaa	gaa	atc	act	336	
Asp	Lys	Val	Gln	Lys	Cys	Ser	His	Tyr	Leu	Phe	Ser	Glu	Glu	Ile	Thr		
			100					105						110			
tct	ggc	tgt	cag	ttg	caa	aaa	aag	gag	atc	cac	ctc	tac	caa	aca	ttt	384	
Ser	Gly	Cys	Gln	Leu	Gln	Lys	Lys	Glu	Ile	His	Leu	Tyr	Gln	Thr	Phe		
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gtt	gtt	cag	ctc	cag	gac	cca	cgg	gaa	ccc	agg	aga	cag	gcc	aca	cag	432	
Val	Val	Gln	Leu	Gln	Asp	Pro	Arg	Glu	Pro	Arg	Arg	Gln	Ala	Thr	Gln		
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atg	cta	aaa	ctg	cag	aat	ctg	gtg	atc	ccc	tgg	gct	cca	gag	aac	cta	480	
Met	Leu	Lys	Leu	Gln	Asn	Leu	Val	Ile	Pro	Trp	Ala	Pro	Glu	Asn	Leu		
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aca	ctt	cac	aaa	ctg	agt	gaa	tcc	cag	cta	gaa	ctg	aac	tgg	aac	aac	528	
Thr	Leu	His	Lys	Leu	Ser	Glu	Ser	Gln	Leu	Glu	Leu	Asn	Trp	Asn	Asn		
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aga	ttc	ttg	aac	cac	tgt	ttg	gag	cac	ttg	gtg	cag	tac	cgg	act	gac	576	
Arg	Phe	Leu	Asn	His	Cys	Leu	Glu	His	Leu	Val	Gln	Tyr	Arg	Thr	Asp		
			180					185							190		
tgg	gac	cac	agc	tgg	act	gaa	caa	tca	gtg	gat	tat	aga	cat	aag	ttc	624	
Trp	Asp	His	Ser	Trp	Thr	Glu	Gln	Ser	Val	Asp	Tyr	Arg	His	Lys	Phe		
		195						200							205		
tcc	ttg	cct	agt	gtg	gat	ggg	cag	aaa	cgc	tac	acg	ttt	cgt	gtt	cgg	672	
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Asn	Glu	Asp	Thr	Thr	Ala	Asp	Phe	Phe	Leu	Thr	Thr	Met	Pro	Thr	Asp
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Ser	Leu	Ser	Val	Ser	Thr	Leu	Pro	Leu	Pro	Glu	Val	Gln	Cys	Phe	Val
	50					55					60				
Phe	Asn	Val	Glu	Tyr	Met	Asn	Cys	Thr	Trp	Asn	Ser	Ser	Ser	Glu	Pro
65					70					75					80
Gln	Pro	Thr	Asn	Leu	Thr	Leu	His	Tyr	Trp	Tyr	Lys	Asn	Ser	Asp	Asn
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Asp	Lys	Val	Gln	Lys	Cys	Ser	His	Tyr	Leu	Phe	Ser	Glu	Glu	Ile	Thr
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Ser	Gly	Cys	Gln	Leu	Gln	Lys	Lys	Glu	Ile	His	Leu	Tyr	Gln	Thr	Phe
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Val	Val	Gln	Leu	Gln	Asp	Pro	Arg	Glu	Pro	Arg	Arg	Gln	Ala	Thr	Gln
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Thr	Leu	His	Lys	Leu	Ser	Glu	Ser	Gln	Leu	Glu	Leu	Asn	Trp	Asn	Asn
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Arg	Phe	Leu	Asn	His	Cys	Leu	Glu	His	Leu	Val	Gln	Tyr	Arg	Thr	Asp
			180					185					190		
Trp	Asp	His	Ser	Trp	Thr	Glu	Gln	Ser	Val	Asp	Tyr	Arg	His	Lys	Phe
		195				200					205				
Ser	Leu	Pro	Ser	Val	Asp	Gly	Gln	Lys	Arg	Tyr	Thr	Phe	Arg	Val	Arg
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Ser	Arg	Phe	Asn	Pro	Leu	Cys	Gly	Ser	Ala	Gln	His	Trp	Ser	Glu	Trp
225					230					235					240
Ser	His	Pro	Ile	His	Trp	Gly	Ser	Asn	Thr	Ser	Lys	Glu	Asn	Thr	Val
			245					250					255		
Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys
		260					265						270		
Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg
		275				280						285			
Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn
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36

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<400> 23
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<210> 24
 <211> 66
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer spanning vector flanking
 region and the 5' end of the zalpha11

<400> 24
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 ggccgc 66

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 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180

aactggtacg	tggacggcgt	ggaggtgcat	aatgccaa	caaagccgcg	ggaggagcag	240
tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgcaccagga	ctggctgaat	300
ggcaaggagt	acaagtgcaa	ggtctccaac	aaagccctcc	catcctccat	cgagaaaacc	360
atctccaaag	ccaaagggca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatcccgg	420
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aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	660
tacacgcaga	agagcctctc	cctgtctccg	ggtaaataa			699

<210> 26

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<212> DNA

<213> Artificial Sequence

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<223> First Oligonucleotide primer spanning 3' end of
the zalpha11 extracellular domain and the 5' end
of Fc4

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<210> 27

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Second Oligonucleotide primer spanning 3' end of
the zalpha11 extracellular domain and the 5' end
of Fc4

<400> 27

agaccagtc	agaggagtta	aaggaaggct	ggaaccctca	cgagcccaga	tcttcagaca	60
a						61

<210> 28

<211> 67

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer spanning the 3' end of Fc4
and the vector flanking region

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acagggga	67

<210> 29

<211> 1821

<212> DNA

<213> Artificial Sequence

<220>

<223> Polynucleotide encoding MBP-human zalpha11 soluble
receptor fusion

<221> CDS

<222> (1)...(1821)

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1 5 10 15	

ggc tat aac ggt ctc gct gaa gtc ggt aag aaa ttc gag aaa gat acc	96
Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr	
20 25 30	

gga att aaa gtc acc gtt gag cat ccg gat aaa ctg gaa gag aaa ttc	144
Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe	
35 40 45	

cca cag gtt gcg gca act ggc gat ggc cct gac att atc ttc tgg gca	192
Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala	
50 55 60	

cac gac cgc ttt ggt ggc tac gct caa tct ggc ctg ttg gct gaa atc	240
His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile	
65 70 75 80	

acc ccg gac aaa gcg ttc cag gac aag ctg tat ccg ttt acc tgg gat	288
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Thr	Pro	Asp	Lys	Ala	Phe	Gln	Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp	
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gcc	gta	cgt	tac	aac	ggc	aag	ctg	att	gct	tac	ccg	atc	gct	gtt	gaa	336
Ala	Val	Arg	Tyr	Asn	Gly	Lys	Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu	
			100				105					110				
gcg	tta	tcg	ctg	att	tat	aac	aaa	gat	ctg	ctg	ccg	aac	ccg	cca	aaa	384
Ala	Leu	Ser	Leu	Ile	Tyr	Asn	Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys	
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acc	tgg	gaa	gag	atc	ccg	gcg	ctg	gat	aaa	gaa	ctg	aaa	gcg	aaa	ggt	432
Thr	Trp	Glu	Glu	Ile	Pro	Ala	Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	
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aag	agc	gcg	ctg	atg	ttc	aac	ctg	caa	gaa	ccg	tac	ttc	acc	tgg	ccg	480
Lys	Ser	Ala	Leu	Met	Phe	Asn	Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	
		145				150				155					160	
ctg	att	gct	gct	gac	ggg	ggt	tat	gcg	ttc	aag	tat	gaa	aac	ggc	aag	528
Leu	Ile	Ala	Ala	Asp	Gly	Gly	Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys	
				165				170						175		
tac	gac	att	aaa	gac	gtg	ggc	gtg	gat	aac	gct	ggc	gcg	aaa	gcg	ggt	576
Tyr	Asp	Ile	Lys	Asp	Val	Gly	Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	
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ctg	acc	ttc	ctg	gtt	gac	ctg	att	aaa	aac	aaa	cac	atg	aat	gca	gac	624
Leu	Thr	Phe	Leu	Val	Asp	Leu	Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	
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acc	gat	tac	tcc	atc	gca	gaa	gct	gcc	ttt	aat	aaa	ggc	gaa	aca	gcg	672
Thr	Asp	Tyr	Ser	Ile	Ala	Glu	Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	
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gtg	aat	tat	ggt	gta	acg	gta	ctg	ccg	acc	ttc	aag	ggt	caa	cca	tcc	768
Val	Asn	Tyr	Gly	Val	Thr	Val	Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	
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aaa ccg ttc gtt ggc gtg ctg agc gca ggt att aac gcc gcc agt ccg	816
Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro	
260 265 270	
aac aaa gag ctg gca aaa gag ttc ctc gaa aac tat ctg ctg act gat	864
Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp	
275 280 285	
gaa ggt ctg gaa gcg gtt aat aaa gac aaa ccg ctg ggt gcc gta gcg	912
Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala	
290 295 300	
ctg aag tct tac gag gaa gag ttg gcg aaa gat cca cgt att gcc gcc	960
Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala	
305 310 315 320	
acc atg gaa aac gcc cag aaa ggt gaa atc atg ccg aac atc ccg cag	1008
Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln	
325 330 335	
atg tcc gct ttc tgg tat gcc gtg cgt act gcg gtg atc aac gcc gcc	1056
Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala	
340 345 350	
agc ggt cgt cag act gtc gat gaa gcc ctg aaa gac gcg cag act aat	1104
Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn	
355 360 365	
tcg agc tcc cac cat cac cat cac cac gcg aat tcg gta ccg ctg gtt	1152
Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu Val	
370 375 380	
ccg cgt gga tcc tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag	1200
Pro Arg Gly Ser Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln	
385 390 395 400	
acg gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc	1248
Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu	
405 410 415	
acc ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc	1296

Thr	Leu	Thr	Trp	Gln	Asp	Gln	Tyr	Glu	Glu	Leu	Lys	Asp	Glu	Ala	Thr	
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Ser	Cys	Ser	Leu	His	Arg	Ser	Ala	His	Asn	Ala	Thr	His	Ala	Thr	Tyr	
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Thr	Cys	His	Met	Asp	Val	Phe	His	Phe	Met	Ala	Asp	Asp	Ile	Phe	Ser	
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gtc	aac	atc	aca	gac	cag	tct	ggc	aac	tac	tcc	cag	gag	tgt	ggc	agc	1440
Val	Asn	Ile	Thr	Asp	Gln	Ser	Gly	Asn	Tyr	Ser	Gln	Glu	Cys	Gly	Ser	
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Phe	Leu	Leu	Ala	Glu	Ser	Ile	Lys	Pro	Ala	Pro	Pro	Phe	Asn	Val	Thr	
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gtg	acc	ttc	tca	gga	cag	tat	aat	atc	tcc	tgg	cgc	tca	gat	tac	gaa	1536
Val	Thr	Phe	Ser	Gly	Gln	Tyr	Asn	Ile	Ser	Trp	Arg	Ser	Asp	Tyr	Glu	
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gac	cct	gcc	ttc	tac	atg	ctg	aag	ggc	aag	ctt	cag	tat	gag	ctg	cag	1584
Asp	Pro	Ala	Phe	Tyr	Met	Leu	Lys	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln	
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Tyr	Arg	Asn	Arg	Gly	Asp	Pro	Trp	Ala	Val	Ser	Pro	Arg	Arg	Lys	Leu	
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atc	tca	gtg	gac	tca	aga	agt	gtc	tcc	ctc	ctc	ccc	ctg	gag	ttc	cgc	1680
Ile	Ser	Val	Asp	Ser	Arg	Ser	Val	Ser	Leu	Leu	Pro	Leu	Glu	Phe	Arg	
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aaa	gac	tcg	agc	tat	gag	ctg	cag	gtg	cgg	gca	ggg	ccc	atg	cct	ggc	1728
Lys	Asp	Ser	Ser	Tyr	Glu	Leu	Gln	Val	Arg	Ala	Gly	Pro	Met	Pro	Gly	
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tcc	tcc	tac	cag	ggg	acc	tgg	agt	gaa	tgg	agt	gac	ccg	gtc	atc	ttt	1776
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1821

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His	Asp	Arg	Phe	Gly	Gly	Tyr	Ala	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Ile
65 70 75 80															
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85 90 95															
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130 135 140															
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145 150 155 160															
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165 170 175															
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210 215 220															
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225 230 235 240															
Val	Asn	Tyr	Gly	Val	Thr	Val	Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser
245 250 255															

Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro
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 275 280 285
 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala
 290 295 300
 Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala
 305 310 315 320
 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln
 325 330 335
 Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala
 340 345 350
 Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn
 355 360 365
 Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu Val
 370 375 380
 Pro Arg Gly Ser Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln
 385 390 395 400
 Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu
 405 410 415
 Thr Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr
 420 425 430
 Ser Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr
 435 440 445
 Thr Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser
 450 455 460
 Val Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser
 465 470 475 480
 Phe Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr
 485 490 495
 Val Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu
 500 505 510
 Asp Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln
 515 520 525
 Tyr Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu
 530 535 540
 Ile Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg
 545 550 555 560
 Lys Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly
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 Ser Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe
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104

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152

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248

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344

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 50         55         60
Glu His Ala Ala Phe Ala Cys Phe Gln Lys Ala Lys Leu Lys Pro Ser
 65         70         75         80
Asn Pro Gly Asn Asn Lys Thr Phe Ile Ile Asp Leu Val Ala Gln Leu
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Ala Lys Cys Pro Ser Cys Asp Ser Tyr Glu Lys Arg Thr Pro Lys Glu
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Thr Lys Ala Ser Leu Pro Thr Asp Pro Pro Gly Trp Gly Cys Pro Asp
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Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr Val Ile Cys Ile Leu Glu
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 Ser Arg Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala
 165 170 175
 Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn
 180 185 190
 Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val
 195 200 205
 Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser
 210 215 220
 Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr
 225 230 235 240
 Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln
 245 250 255
 Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu Leu Leu
 260 265 270
 Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys Thr His
 275 280 285
 Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser Pro Glu
 290 295 300
 Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe Lys Lys
 305 310 315 320
 Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly Pro Trp
 325 330 335
 Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His Pro Pro
 340 345 350
 Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu Pro Ala
 355 360 365

Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp Pro Thr
 370 375 380
 Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp Arg Pro
 385 390 395 400
 Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala Glu Gly
 405 410 415
 Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro Ala Leu
 420 425 430
 Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp Pro Leu
 435 440 445
 Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser Ala Gly
 450 455 460
 Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg Leu Lys
 465 470 475 480
 Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro Trp Gly
 485 490 495
 Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser Pro Leu
 500 505 510
 Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly Ser Asp
 515 520 525
 Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp Glu Gly
 530 535 540
 Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro Pro Leu
 545 550 555 560
 Ser Ser Pro Gly Pro Gln Ala Ser
 565

<210> 66

<211> 741

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate polynucleotide sequence of SEQ ID NO:69

<221> misc_feature

<222> (1)...(741)

<223> n = A,T,C or G

<400> 66

atggarmgna arytnntyws nccnaarccn ccncnacna argcnwsnyt nccnacngay 60
 ccnccnggnt ggggntgycc ngayyngtn tgytayacng aytayytnc racngtnath 120

tgyathytn	aratgtggaa	yytncaayccn	wsnacnytna	cnytnacntg	gathytnwsn	180
aayaayacng	gntgytayat	haargaymgn	acnytngayy	tnmgncarga	ycartaygar	240
garytnaarg	aygargcnac	nwsntgywsn	ytncaymgnw	sngcncayaa	ycnacncay	300
gcnacntaya	cntgycayat	ggaygtntty	cayttyatgg	cngaygayat	httywsngtn	360
aayathacng	aycarwsngg	naaytaywsn	cargartgyg	gnwsnttyyt	nytngcngar	420
wsnmgncart	ayaayathws	ntggmgwnsn	gaytaygarg	ayccngcntt	ytayatgytn	480
aarggnaary	tncartayga	rytncartay	mgnaaymgng	gngayccntg	ggcngtnwsn	540
ccnmgmngna	arytnathws	ngtngaywsn	mgnwsngtnw	snytnytncc	nytngartty	600
mgnaargayw	snwsntayga	rytncargtn	mgngcnggnc	cnatgccngg	nwsnwsntay	660
carggnacnt	ggwsngartg	gwsngayccn	gtnathttyc	aracncarws	ngargarytn	720
aargarggnt	ggaayccnca	y				741

<210> 67

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> WXXW motif

<221> VARIANT

<222> (1)...(4)

<223> Xaa = Any Amino Acid

<400> 67

Trp Xaa Xaa Trp

1

<210> 68

<211> 741

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(741)

<400> 68

atg	gag	agg	aag	ctc	tgc	agt	ccc	aag	cca	ccc	ccc	acc	aag	gcc	tct	48
Met	Glu	Arg	Lys	Leu	Cys	Ser	Pro	Lys	Pro	Pro	Pro	Thr	Lys	Ala	Ser	
1				5				10						15		

ctc	ccc	act	gac	cct	cca	ggc	tgg	ggc	tgc	ccc	gac	ctc	gtc	tgc	tac	96
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----

Leu	Pro	Thr	Asp	Pro	Pro	Gly	Trp	Gly	Cys	Pro	Asp	Leu	Val	Cys	Tyr	
			20					25					30			
acc	gat	tac	ctc	cag	acg	gtc	atc	tgc	atc	ctg	gaa	atg	tgg	aac	ctc	144
Thr	Asp	Tyr	Leu	Gln	Thr	Val	Ile	Cys	Ile	Leu	Glu	Met	Trp	Asn	Leu	
		35					40				45					
cac	ccc	agc	acg	ctc	acc	ctt	acc	tgg	ata	ctt	tct	aat	aat	act	ggg	192
His	Pro	Ser	Thr	Leu	Thr	Leu	Thr	Trp	Ile	Leu	Ser	Asn	Asn	Thr	Gly	
	50					55					60					
tgc	tat	atc	aag	gac	aga	aca	ctg	gac	ctc	agg	caa	gac	cag	tat	gaa	240
Cys	Tyr	Ile	Lys	Asp	Arg	Thr	Leu	Asp	Leu	Arg	Gln	Asp	Gln	Tyr	Glu	
65					70				75						80	
gag	ctg	aag	gac	gag	gcc	acc	tcc	tgc	agc	ctc	cac	agg	tcg	gcc	cac	288
Glu	Leu	Lys	Asp	Glu	Ala	Thr	Ser	Cys	Ser	Leu	His	Arg	Ser	Ala	His	
				85				90						95		
aat	gcc	acg	cat	gcc	acc	tac	acc	tgc	cac	atg	gat	gta	ttc	cac	ttc	336
Asn	Ala	Thr	His	Ala	Thr	Tyr	Thr	Cys	His	Met	Asp	Val	Phe	His	Phe	
			100					105					110			
atg	gcc	gac	gac	att	ttc	agt	gtc	aac	atc	aca	gac	cag	tct	ggc	aac	384
Met	Ala	Asp	Asp	Ile	Phe	Ser	Val	Asn	Ile	Thr	Asp	Gln	Ser	Gly	Asn	
		115					120					125				
tac	tcc	cag	gag	tgt	ggc	agc	ttt	ctc	ctg	gct	gag	agc	aga	cag	tat	432
Tyr	Ser	Gln	Glu	Cys	Gly	Ser	Phe	Leu	Leu	Ala	Glu	Ser	Arg	Gln	Tyr	
	130					135					140					
aat	atc	tcc	tgg	cgc	tca	gat	tac	gaa	gac	cct	gcc	ttc	tac	atg	ctg	480
Asn	Ile	Ser	Trp	Arg	Ser	Asp	Tyr	Glu	Asp	Pro	Ala	Phe	Tyr	Met	Leu	
145				150					155					160		
aag	ggc	aag	ctt	cag	tat	gag	ctg	cag	tac	agg	aac	cgg	gga	gac	ccc	528
Lys	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln	Tyr	Arg	Asn	Arg	Gly	Asp	Pro	
			165					170					175			
tgg	gct	gtg	agt	ccg	agg	aga	aag	ctg	atc	tca	gtg	gac	tca	aga	agt	576
Trp	Ala	Val	Ser	Pro	Arg	Arg	Lys	Leu	Ile	Ser	Val	Asp	Ser	Arg	Ser	
			180					185					190			

Met 1	Glu	Arg	Lys	Leu 5	Cys	Ser	Pro	Lys	Pro 10	Pro	Pro	Thr	Lys	Ala 15	Ser
Leu	Pro	Thr	Asp 20	Pro	Pro	Gly	Trp	Gly 25	Cys	Pro	Asp	Leu	Val 30	Cys	Tyr
Thr	Asp	Tyr	Leu	Gln	Thr	Val	Ile 40	Cys	Ile	Leu	Glu	Met 45	Trp	Asn	Leu
His 50	Pro	Ser	Thr	Leu	Thr	Leu	Thr 55	Trp	Ile	Leu	Ser 60	Asn	Asn	Thr	Gly
Cys 65	Tyr	Ile	Lys	Asp	Arg	Thr	Leu	Asp	Leu	Arg 75	Gln	Asp	Gln	Tyr	Glu 80
Glu	Leu	Lys	Asp	Glu	Ala	Thr	Ser	Cys	Ser 90	Leu	His	Arg	Ser	Ala 95	His
Asn	Ala	Thr	His 100	Ala	Thr	Tyr	Thr	Cys 105	His	Met	Asp	Val	Phe 110	His	Phe
Met	Ala	Asp	Asp	Ile	Phe	Ser	Val 120	Asn	Ile	Thr	Asp 125	Gln	Ser	Gly	Asn
Tyr	Ser	Gln	Glu	Cys	Gly	Ser 135	Phe	Leu	Leu	Ala	Glu 140	Ser	Arg	Gln	Tyr
Asn 145	Ile	Ser	Trp	Arg	Ser	Asp	Tyr	Glu	Asp 155	Pro	Ala	Phe	Tyr	Met	Leu 160

Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg Gly Asp Pro
 165 170 175
 Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp Ser Arg Ser
 180 185 190
 Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser Tyr Glu Leu
 195 200 205
 Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln Gly Thr Trp
 210 215 220
 Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser Glu Glu Leu
 225 230 235 240
 Lys Glu Gly Trp Asn Pro His
 245

<210> 70

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Domain linker motif; PAPP motif

<400> 70

Pro Ala Pro Pro

1

<210> 71

<211> 261

<212> PRT

<213> Artificial Sequence

<220>

<223> Representative variant soluble receptor with
domain linker

<221> VARIANT

<222> (1)...(261)

<223> Xaa = Any Amino Acid

<400> 71

Met Glu Arg Lys Leu Cys Ser Pro Lys Pro Pro Pro Thr Lys Ala Ser

1

5

10

15

Leu Pro Thr Asp Pro Pro Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr
 20 25 30
 Thr Asp Tyr Leu Gln Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu
 35 40 45
 His Pro Ser Thr Leu Thr Leu Thr Trp Ile Leu Ser Asn Asn Thr Gly
 50 55 60
 Cys Tyr Ile Lys Asp Arg Thr Leu Asp Leu Arg Gln Asp Gln Tyr Glu
 65 70 75 80
 Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu His Arg Ser Ala His
 85 90 95
 Asn Ala Thr His Ala Thr Tyr Thr Cys His Met Asp Val Phe His Phe
 100 105 110
 Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr Asp Gln Ser Gly Asn
 115 120 125
 Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala Glu Ser Xaa Xaa Pro
 130 135 140
 Ala Pro Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Gln Tyr Asn Ile
 145 150 155 160
 Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe Tyr Met Leu Lys Gly
 165 170 175
 Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg Gly Asp Pro Trp Ala
 180 185 190
 Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp Ser Arg Ser Val Ser
 195 200 205
 Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser Tyr Glu Leu Gln Val
 210 215 220
 Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln Gly Thr Trp Ser Glu
 225 230 235 240
 Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser Glu Glu Leu Lys Glu
 245 250 255
 Gly Trp Asn Pro His
 260

<210> 72

<211> 1461

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse zalpha11 extracellular domain murine
 immunoglobulin gamma 2a heavy chain Fc region
 fusion protein (zalpha11m-mG2a) Polynucleotide

<221> CDS

<222> (1)...(1461)

<400> 72

atg	gat	gca	atg	aag	aga	ggg	ctc	tgc	tgt	gtg	ctg	ctg	ctg	tgt	ggc	48
Met	Asp	Ala	Met	Lys	Arg	Gly	Leu	Cys	Cys	Val	Leu	Leu	Leu	Cys	Gly	
1				5				10						15		

gcc	gtc	ttc	gtt	tcg	ctc	agc	cag	aaa	atc	cat	gcc	gag	ttg	aga	cgc	96
Ala	Val	Phe	Val	Ser	Leu	Ser	Gln	Lys	Ile	His	Ala	Glu	Leu	Arg	Arg	
			20					25					30			

ttc	cgg	aga	tgc	ctg	gac	ctc	act	tgc	tac	act	gac	tac	ctc	tgg	acc	144
Phe	Arg	Arg	Cys	Leu	Asp	Leu	Thr	Cys	Tyr	Thr	Asp	Tyr	Leu	Trp	Thr	
			35				40					45				

atc	acc	tgt	gtc	ctg	gag	aca	cgg	agc	ccc	aac	ccc	agc	ata	ctc	agt	192
Ile	Thr	Cys	Val	Leu	Glu	Thr	Arg	Ser	Pro	Asn	Pro	Ser	Ile	Leu	Ser	
			50				55				60					

ctc	acc	tgg	caa	gat	gaa	tat	gag	gaa	ctt	cag	gac	caa	gag	acc	ttc	240
Leu	Thr	Trp	Gln	Asp	Glu	Tyr	Glu	Glu	Leu	Gln	Asp	Gln	Glu	Thr	Phe	
			65			70				75					80	

tgc	agc	cta	cac	agg	tct	ggc	cac	aac	acc	aca	cat	ata	tgg	tac	acg	288
Cys	Ser	Leu	His	Arg	Ser	Gly	His	Asn	Thr	Thr	His	Ile	Trp	Tyr	Thr	
				85					90					95		

tgc	cat	atg	cgc	ttg	tct	caa	ttc	ctg	tcc	gat	gaa	gtt	ttc	att	gtc	336
Cys	His	Met	Arg	Leu	Ser	Gln	Phe	Leu	Ser	Asp	Glu	Val	Phe	Ile	Val	
			100					105					110			

aat	gtg	acg	gac	cag	tct	ggc	aac	aac	tcc	caa	gag	tgt	ggc	agc	ttt	384
Asn	Val	Thr	Asp	Gln	Ser	Gly	Asn	Asn	Ser	Gln	Glu	Cys	Gly	Ser	Phe	
			115				120					125				

gtc	ctg	gct	gag	agc	atc	aaa	cca	gct	ccc	ccc	ttg	aac	gtg	act	gtg	432
Val	Leu	Ala	Glu	Ser	Ile	Lys	Pro	Ala	Pro	Pro	Leu	Asn	Val	Thr	Val	
			130				135				140					

gcc	ttc	tca	gga	cgc	tat	gat	atc	tcc	tgg	gac	tca	gct	tat	gac	gaa	480
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Ala	Phe	Ser	Gly	Arg	Tyr	Asp	Ile	Ser	Trp	Asp	Ser	Ala	Tyr	Asp	Glu	
145					150				155					160		
ccc	tcc	aac	tac	gtg	ctg	agg	ggc	aag	cta	caa	tat	gag	ctg	cag	tat	528
Pro	Ser	Asn	Tyr	Val	Leu	Arg	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln	Tyr	
				165				170						175		
cgg	aac	ctc	aga	gac	ccc	tat	gct	gtg	agg	ccg	gtg	acc	aag	ctg	atc	576
Arg	Asn	Leu	Arg	Asp	Pro	Tyr	Ala	Val	Arg	Pro	Val	Thr	Lys	Leu	Ile	
			180					185					190			
tca	gtg	gac	tca	aga	aac	gtc	tct	ctt	ctc	cct	gaa	gag	ttc	cac	aaa	624
Ser	Val	Asp	Ser	Arg	Asn	Val	Ser	Leu	Leu	Pro	Glu	Glu	Phe	His	Lys	
		195					200					205				
gat	tct	agc	tac	cag	ctg	cag	gtg	cgg	gca	gcg	cct	cag	cca	ggc	act	672
Asp	Ser	Ser	Tyr	Gln	Leu	Gln	Val	Arg	Ala	Ala	Pro	Gln	Pro	Gly	Thr	
	210					215					220					
tca	ttc	agg	ggg	acc	tgg	agt	gag	tgg	agt	gac	ccc	gtc	atc	ttt	cag	720
Ser	Phe	Arg	Gly	Thr	Trp	Ser	Glu	Trp	Ser	Asp	Pro	Val	Ile	Phe	Gln	
225					230					235					240	
acc	cag	gct	ggg	gag	ccc	gag	gca	ggc	tgg	gac	cct	cac	gag	ccc	aga	768
Thr	Gln	Ala	Gly	Glu	Pro	Glu	Ala	Gly	Trp	Asp	Pro	His	Glu	Pro	Arg	
			245						250					255		
tct	ccc	aca	atc	aag	ccc	tgt	cct	cca	tgc	aaa	tgc	cca	gca	cct	aac	816
Ser	Pro	Thr	Ile	Lys	Pro	Cys	Pro	Pro	Cys	Lys	Cys	Pro	Ala	Pro	Asn	
			260					265					270			
ctc	ttg	ggt	gga	cca	tcc	gtc	ttc	atc	ttc	cct	cca	aag	atc	aag	gat	864
Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Ile	Lys	Asp	
		275					280					285				
gta	ctc	atg	atc	tcc	ctg	agc	ccc	ata	gtc	aca	tgt	gtg	gtg	gtg	gat	912
Val	Leu	Met	Ile	Ser	Leu	Ser	Pro	Ile	Val	Thr	Cys	Val	Val	Val	Asp	
		290				295					300					
gtg	agc	gag	gat	gac	cca	gat	gtc	cag	atc	agc	tgg	ttt	gtg	aac	aac	960
Val	Ser	Glu	Asp	Asp	Pro	Asp	Val	Gln	Ile	Ser	Trp	Phe	Val	Asn	Asn	
305					310					315				320		

gtg gaa gta cac aca gct cag aca caa acc cat aga gag gat tac aac	1008
Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn	
325 330 335	
agt act ctc cgg gtg gtc agt gcc ctc ccc atc cag cac cag gac tgg	1056
Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp	
340 345 350	
atg agt ggc aag gag ttc aaa tgc aag gtc aac aac aaa gac ctc cca	1104
Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro	
355 360 365	
gcg ccc atc gag aga acc atc tca aaa ccc aaa ggg tca gta aga gct	1152
Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala	
370 375 380	
cca cag gta tat gtc ttg cct cca cca gaa gaa gag atg act aag aaa	1200
Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys	
385 390 395 400	
cag gtc act ctg acc tgc atg gtc aca gac ttc atg cct gaa gac att	1248
Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile	
405 410 415	
tac gtg gag tgg acc aac aac ggg aaa aca gag cta aac tac aag aac	1296
Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn	
420 425 430	
act gaa cca gtc ctg gac tct gat ggt tct tac ttc atg tac agc aag	1344
Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys	
435 440 445	
ctg aga gtg gaa aag aag aac tgg gtg gaa aga aat agc tac tcc tgt	1392
Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys	
450 455 460	
tca gtg gtc cac gag ggt ctg cac aat cac cac acg act aag agc ttc	1440
Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe	
465 470 475 480	
tcc cgg act ccg ggt aaa taa	1461

Ser Arg Thr Pro Gly Lys *
485

<210> 73
<211> 486
<212> PRT
<213> Artificial Sequence

<400> 73

Met	Asp	Ala	Met	Lys	Arg	Gly	Leu	Cys	Cys	Val	Leu	Leu	Leu	Cys	Gly
1				5				10						15	
Ala	Val	Phe	Val	Ser	Leu	Ser	Gln	Lys	Ile	His	Ala	Glu	Leu	Arg	Arg
			20					25					30		
Phe	Arg	Arg	Cys	Leu	Asp	Leu	Thr	Cys	Tyr	Thr	Asp	Tyr	Leu	Trp	Thr
	35						40					45			
Ile	Thr	Cys	Val	Leu	Glu	Thr	Arg	Ser	Pro	Asn	Pro	Ser	Ile	Leu	Ser
	50						55				60				
Leu	Thr	Trp	Gln	Asp	Glu	Tyr	Glu	Glu	Leu	Gln	Asp	Gln	Glu	Thr	Phe
65				70						75				80	
Cys	Ser	Leu	His	Arg	Ser	Gly	His	Asn	Thr	Thr	His	Ile	Trp	Tyr	Thr
			85					90					95		
Cys	His	Met	Arg	Leu	Ser	Gln	Phe	Leu	Ser	Asp	Glu	Val	Phe	Ile	Val
			100					105					110		
Asn	Val	Thr	Asp	Gln	Ser	Gly	Asn	Asn	Ser	Gln	Glu	Cys	Gly	Ser	Phe
			115				120					125			
Val	Leu	Ala	Glu	Ser	Ile	Lys	Pro	Ala	Pro	Pro	Leu	Asn	Val	Thr	Val
	130					135					140				
Ala	Phe	Ser	Gly	Arg	Tyr	Asp	Ile	Ser	Trp	Asp	Ser	Ala	Tyr	Asp	Glu
145				150						155				160	
Pro	Ser	Asn	Tyr	Val	Leu	Arg	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln	Tyr
			165					170						175	
Arg	Asn	Leu	Arg	Asp	Pro	Tyr	Ala	Val	Arg	Pro	Val	Thr	Lys	Leu	Ile
		180					185						190		
Ser	Val	Asp	Ser	Arg	Asn	Val	Ser	Leu	Leu	Pro	Glu	Glu	Phe	His	Lys
	195					200					205				
Asp	Ser	Ser	Tyr	Gln	Leu	Gln	Val	Arg	Ala	Ala	Pro	Gln	Pro	Gly	Thr
	210				215						220				
Ser	Phe	Arg	Gly	Thr	Trp	Ser	Glu	Trp	Ser	Asp	Pro	Val	Ile	Phe	Gln
225				230					235					240	
Thr	Gln	Ala	Gly	Glu	Pro	Glu	Ala	Gly	Trp	Asp	Pro	His	Glu	Pro	Arg
			245					250						255	

Ser Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn
 260 265 270
 Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp
 275 280 285
 Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp
 290 295 300
 Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn
 305 310 315 320
 Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn
 325 330 335
 Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp
 340 345 350
 Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro
 355 360 365
 Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala
 370 375 380
 Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys
 385 390 395 400
 Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile
 405 410 415
 Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn
 420 425 430
 Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys
 435 440 445
 Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys
 450 455 460
 Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe
 465 470 475 480
 Ser Arg Thr Pro Gly Lys
 485

<210> 74

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC26644

<400> 74

ggggtcgacg gccggccacc atg

<210> 75
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC26641

<400> 75
 caagtgaggt ccaggcatct ccggaagcgt ctcaa 35

<210> 76
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC26642

<400> 76
 ttgagacgct tccggagatg cctggacctc acttg 35

<210> 77
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC26662

<400> 77
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<210> 78
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC26643

<400> 78
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<210> 79
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC26645

<400> 79
 aaacgcggcc gcgatccgg c 21

<210> 80
 <211> 35
 <212> PRT
 <213> Homo sapeins

<400> 80
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 Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg
 20 25 30
 Phe Arg Arg
 35

<210> 81
 <211> 966
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(966)

<400> 81
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 Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn
 1 5 10 15
 ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata tgg aca tgg aat 96
 Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn
 20 25 30

cca	ccc	gag	gga	gcc	agc	tca	aat	tgt	agt	cta	tgg	tat	ttt	agt	cat	144
Pro	Pro	Glu	Gly	Ala	Ser	Ser	Asn	Cys	Ser	Leu	Trp	Tyr	Phe	Ser	His	
		35					40					45				
ttt	ggc	gac	aaa	caa	gat	aag	aaa	ata	gct	ccg	gaa	act	cgt	cgt	tca	192
Phe	Gly	Asp	Lys	Gln	Asp	Lys	Lys	Ile	Ala	Pro	Glu	Thr	Arg	Arg	Ser	
	50					55					60					
ata	gaa	gta	ccc	ctg	aat	gag	agg	att	tgt	ctg	caa	gtg	ggg	tcc	cag	240
Ile	Glu	Val	Pro	Leu	Asn	Glu	Arg	Ile	Cys	Leu	Gln	Val	Gly	Ser	Gln	
65					70					75					80	
tgt	agc	acc	aat	gag	agt	gag	aag	cct	agc	att	ttg	gtt	gaa	aaa	tgc	288
Cys	Ser	Thr	Asn	Glu	Ser	Glu	Lys	Pro	Ser	Ile	Leu	Val	Glu	Lys	Cys	
				85					90					95		
atc	tca	ccc	cca	gaa	ggc	gat	cct	gag	tct	gct	gtg	act	gag	ctt	caa	336
Ile	Ser	Pro	Pro	Glu	Gly	Asp	Pro	Glu	Ser	Ala	Val	Thr	Glu	Leu	Gln	
			100					105					110			
tgc	att	tgg	cac	aac	ctg	agc	tac	atg	aag	tgt	tct	tgg	ctc	cct	gga	384
Cys	Ile	Trp	His	Asn	Leu	Ser	Tyr	Met	Lys	Cys	Ser	Trp	Leu	Pro	Gly	
		115					120					125				
agg	aat	acc	agt	ccc	gac	act	aac	tat	act	ctc	tac	tat	tgg	cac	aga	432
Arg	Asn	Thr	Ser	Pro	Asp	Thr	Asn	Tyr	Thr	Leu	Tyr	Tyr	Trp	His	Arg	
		130					135				140					
agc	ctg	gaa	aaa	att	cat	caa	tgt	gaa	aac	atc	ttt	aga	gaa	ggc	caa	480
Ser	Leu	Glu	Lys	Ile	His	Gln	Cys	Glu	Asn	Ile	Phe	Arg	Glu	Gly	Gln	
145					150					155					160	
tac	ttt	ggc	tgt	tcc	ttt	gat	ctg	acc	aaa	gtg	aag	gat	tcc	agt	ttt	528
Tyr	Phe	Gly	Cys	Ser	Phe	Asp	Leu	Thr	Lys	Val	Lys	Asp	Ser	Ser	Phe	
				165					170					175		
gaa	caa	cac	agt	gtc	caa	ata	atg	gtc	aag	gat	aat	gca	gga	aaa	att	576
Glu	Gln	His	Ser	Val	Gln	Ile	Met	Val	Lys	Asp	Asn	Ala	Gly	Lys	Ile	
			180					185					190			
aaa	cca	tcc	ttc	aat	ata	gtg	cct	tta	act	tcc	cgt	gtg	aaa	cct	gat	624
Lys	Pro	Ser	Phe	Asn	Ile	Val	Pro	Leu	Thr	Ser	Arg	Val	Lys	Pro	Asp	
		195					200					205				

cct cca cat att aaa aac ctc tcc ttc cac aat gat gac cta tat gtg 672
 Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp Asp Leu Tyr Val
 210 215 220

caa tgg gag aat cca cag aat ttt att agc aga tgc cta ttt tat gaa 720
 Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys Leu Phe Tyr Glu
 225 230 235 240

gta gaa gtc aat aac agc caa act gag aca cat aat gtt ttc tac gtc 768
 Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn Val Phe Tyr Val
 245 250 255

caa gag gct aaa tgt gag aat cca gaa ttt gag aga aat gtg gag aat 816
 Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg Asn Val Glu Asn
 260 265 270

aca tct tgt ttc atg gtc cct ggt gtt ctt cct gat act ttg aac aca 864
 Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr
 275 280 285

gtc aga ata aga gtc aaa aca aat aag tta tgc tat gag gat gac aaa 912
 Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys
 290 295 300

ctc tgg agt aat tgg agc caa gaa atg agt ata ggt aag aag cgc aat 960
 Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly Lys Lys Arg Asn
 305 310 315 320

tcc aca 966
 Ser Thr

<210> 82

<211> 322

<212> PRT

<213> Homo sapiens

<400> 82

Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn
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 Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn
 20 25 30

Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp Tyr Phe Ser His
 35 40 45
 Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu Thr Arg Arg Ser
 50 55 60
 Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln
 65 70 75 80
 Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu Val Glu Lys Cys
 85 90 95
 Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr Glu Leu Gln
 100 105 110
 Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp Leu Pro Gly
 115 120 125
 Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr Tyr Trp His Arg
 130 135 140
 Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe Arg Glu Gly Gln
 145 150 155 160
 Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys Asp Ser Ser Phe
 165 170 175
 Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn Ala Gly Lys Ile
 180 185 190
 Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg Val Lys Pro Asp
 195 200 205
 Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp Asp Leu Tyr Val
 210 215 220
 Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys Leu Phe Tyr Glu
 225 230 235 240
 Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn Val Phe Tyr Val
 245 250 255
 Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg Asn Val Glu Asn
 260 265 270
 Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr
 275 280 285
 Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys
 290 295 300
 Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly Lys Lys Arg Asn
 305 310 315 320
 Ser Thr

<210> 83

<211> 951

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(951)

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ccc gga tac tta ggt tat ctc tat ttg caa tgg caa ccc cca ctg tct	96
Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser	
20 25 30	
ctg gat cat ttt aag gaa tgc aca gtg gaa tat gaa cta aaa tac cga	144
Leu Asp His Phe Lys Glu Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg	
35 40 45	
aac att ggt agt gaa aca tgg aag acc atc att act aag aat cta cat	192
Asn Ile Gly Ser Glu Thr Trp Lys Thr Ile Ile Thr Lys Asn Leu His	
50 55 60	
tac aaa gat ggg ttt gat ctt aac aag ggc att gaa gcg aag ata cac	240
Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu Ala Lys Ile His	
65 70 75 80	
acg ctt tta cca tgg caa tgc aca aat gga tca gaa gtt caa agt tcc	288
Thr Leu Leu Pro Trp Gln Cys Thr Asn Gly Ser Glu Val Gln Ser Ser	
85 90 95	
tgg gca gaa act act tat tgg ata tca cca caa gga att cca gaa act	336
Trp Ala Glu Thr Thr Tyr Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr	
100 105 110	
aaa gtt cag gat atg gat tgc gta tat tac aat tgg caa tat tta ctc	384
Lys Val Gln Asp Met Asp Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu	
115 120 125	
tgt tct tgg aaa cct ggc ata ggt gta ctt ctt gat acc aat tac aac	432
Cys Ser Trp Lys Pro Gly Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn	
130 135 140	
ttg ttt tac tgg tat gag ggc ttg gat cat gca tta cag tgt gtt gat	480

Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ala Leu Gln Cys Val Asp	
145 150 155 160	
tac atc aag gct gat gga caa aat ata gga tgc aga ttt ccc tat ttg	528
Tyr Ile Lys Ala Asp Gly Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu	
165 170 175	
gag gca tca gac tat aaa gat ttc tat att tgt gtt aat gga tca tca	576
Glu Ala Ser Asp Tyr Lys Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser	
180 185 190	
gag aac aag cct atc aga tcc agt tat ttc act ttt cag ctt caa aat	624
Glu Asn Lys Pro Ile Arg Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn	
195 200 205	
ata gtt aaa cct ttg ccg cca gtc tat ctt act ttt act cgg gag agt	672
Ile Val Lys Pro Leu Pro Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser	
210 215 220	
tca tgt gaa att aag ctg aaa tgg agc ata cct ttg gga cct att cca	720
Ser Cys Glu Ile Lys Leu Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro	
225 230 235 240	
gca agg tgt ttt gat tat gaa att gag atc aga gaa gat gat act acc	768
Ala Arg Cys Phe Asp Tyr Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr	
245 250 255	
ttg gtg act gct aca gtt gaa aat gaa aca tac acc ttg aaa aca aca	816
Leu Val Thr Ala Thr Val Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr	
260 265 270	
aat gaa acc cga caa tta tgc ttt gta gta aga agc aaa gtg aat att	864
Asn Glu Thr Arg Gln Leu Cys Phe Val Val Arg Ser Lys Val Asn Ile	
275 280 285	
tat tgc tca gat gac gga att tgg agt gag tgg agt gat aaa caa tgc	912
Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys	
290 295 300	
tgg gaa ggt gaa gac cta tcg aag aaa act ttg cta cgt	951
Trp Glu Gly Glu Asp Leu Ser Lys Lys Thr Leu Leu Arg	
305 310 315	

<210> 84
 <211> 317
 <212> PRT
 <213> Homo sapiens

<400> 84

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			20					25					30		
Leu	Asp	His	Phe	Lys	Glu	Cys	Thr	Val	Glu	Tyr	Glu	Leu	Lys	Tyr	Arg
		35					40					45			
Asn	Ile	Gly	Ser	Glu	Thr	Trp	Lys	Thr	Ile	Ile	Thr	Lys	Asn	Leu	His
	50					55					60				
Tyr	Lys	Asp	Gly	Phe	Asp	Leu	Asn	Lys	Gly	Ile	Glu	Ala	Lys	Ile	His
65				70					75					80	
Thr	Leu	Leu	Pro	Trp	Gln	Cys	Thr	Asn	Gly	Ser	Glu	Val	Gln	Ser	Ser
				85					90					95	
Trp	Ala	Glu	Thr	Thr	Tyr	Trp	Ile	Ser	Pro	Gln	Gly	Ile	Pro	Glu	Thr
			100					105					110		
Lys	Val	Gln	Asp	Met	Asp	Cys	Val	Tyr	Tyr	Asn	Trp	Gln	Tyr	Leu	Leu
		115				120						125			
Cys	Ser	Trp	Lys	Pro	Gly	Ile	Gly	Val	Leu	Leu	Asp	Thr	Asn	Tyr	Asn
		130				135						140			
Leu	Phe	Tyr	Trp	Tyr	Glu	Gly	Leu	Asp	His	Ala	Leu	Gln	Cys	Val	Asp
145					150					155					160
Tyr	Ile	Lys	Ala	Asp	Gly	Gln	Asn	Ile	Gly	Cys	Arg	Phe	Pro	Tyr	Leu
				165					170					175	
Glu	Ala	Ser	Asp	Tyr	Lys	Asp	Phe	Tyr	Ile	Cys	Val	Asn	Gly	Ser	Ser
			180					185					190		
Glu	Asn	Lys	Pro	Ile	Arg	Ser	Ser	Tyr	Phe	Thr	Phe	Gln	Leu	Gln	Asn
		195					200					205			
Ile	Val	Lys	Pro	Leu	Pro	Pro	Val	Tyr	Leu	Thr	Phe	Thr	Arg	Glu	Ser
		210				215						220			
Ser	Cys	Glu	Ile	Lys	Leu	Lys	Trp	Ser	Ile	Pro	Leu	Gly	Pro	Ile	Pro
225					230					235					240
Ala	Arg	Cys	Phe	Asp	Tyr	Glu	Ile	Glu	Ile	Arg	Glu	Asp	Asp	Thr	Thr
				245					250					255	
Leu	Val	Thr	Ala	Thr	Val	Glu	Asn	Glu	Thr	Tyr	Thr	Leu	Lys	Thr	Thr
			260					265					270		
Asn	Glu	Thr	Arg	Gln	Leu	Cys	Phe	Val	Val	Arg	Ser	Lys	Val	Asn	Ile
		275					280						285		

Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys
290 295 300
Trp Glu Gly Glu Asp Leu Ser Lys Lys Thr Leu Leu Arg
305 310 315

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<210> 85
<211> 519
<212> DNA
<213> Homo sapeins
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<220>  
<221> CDS  
<222> (1)...(519)
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Ile	Thr	Cys	Pro	Pro	Pro	Met	Ser	Val	Glu	His	Ala	Asp	Ile	Trp	Val	
1			5			10			15							
aag	agc	tac	agc	ttg	tac	tcc	agg	gag	cgg	tac	att	tgt	aac	tct	ggt	96
Lys	Ser	Tyr	Ser	Leu	Tyr	Ser	Arg	Glu	Arg	Tyr	Ile	Cys	Asn	Ser	Gly	
			20			25			30							
ttc	aag	cgt	aaa	gcc	ggc	acg	tcc	agc	ctg	acg	gag	tgc	gtg	ttg	aac	144
Phe	Lys	Arg	Lys	Ala	Gly	Thr	Ser	Ser	Leu	Thr	Glu	Cys	Val	Leu	Asn	
35			40			45										
aag	gcc	acg	aat	gtc	gcc	cac	tgg	aca	acc	ccc	agt	ctc	aaa	tgc	att	192
Lys	Ala	Thr	Asn	Val	Ala	His	Trp	Thr	Thr	Pro	Ser	Leu	Lys	Cys	Ile	
50			55			60										
aga	gac	cct	gcc	ctg	gtt	cac	caa	agg	cca	gcg	cca	ccc	tcc	aca	gta	240
Arg	Asp	Pro	Ala	Leu	Val	His	Gln	Arg	Pro	Ala	Pro	Pro	Ser	Thr	Val	
65			70			75			80							
acg	acg	gca	ggg	gtg	acc	cca	cag	cca	gag	agc	ctc	tcc	cct	tct	gga	288
Thr	Thr	Ala	Gly	Val	Thr	Pro	Gln	Pro	Glu	Ser	Leu	Ser	Pro	Ser	Gly	
			85			90			95							
aaa	gag	ccc	gca	gct	tca	tct	ccc	agc	tca	aac	aac	aca	gcg	gcc	aca	336
Lys	Glu	Pro	Ala	Ala	Ser	Ser	Pro	Ser	Ser	Asn	Asn	Thr	Ala	Ala	Thr	
100			105			110										

Ile	Thr	Cys	Pro	Pro	Pro	Met	Ser	Val	Glu	His	Ala	Asp	Ile	Trp	Val
1				5				10					15		
Lys	Ser	Tyr	Ser	Leu	Tyr	Ser	Arg	Glu	Arg	Tyr	Ile	Cys	Asn	Ser	Gly
			20					25					30		
Phe	Lys	Arg	Lys	Ala	Gly	Thr	Ser	Ser	Leu	Thr	Glu	Cys	Val	Leu	Asn
		35					40					45			
Lys	Ala	Thr	Asn	Val	Ala	His	Trp	Thr	Thr	Pro	Ser	Leu	Lys	Cys	Ile
	50					55				60					
Arg	Asp	Pro	Ala	Leu	Val	His	Gln	Arg	Pro	Ala	Pro	Pro	Ser	Thr	Val
65				70					75						80
Thr	Thr	Ala	Gly	Val	Thr	Pro	Gln	Pro	Glu	Ser	Leu	Ser	Pro	Ser	Gly
			85					90						95	
Lys	Glu	Pro	Ala	Ala	Ser	Ser	Pro	Ser	Ser	Asn	Asn	Thr	Ala	Ala	Thr
			100					105					110		
Thr	Ala	Ala	Ile	Val	Pro	Gly	Ser	Gln	Leu	Met	Pro	Ser	Lys	Ser	Pro
		115					120					125			
Ser	Thr	Gly	Thr	Thr	Glu	Ile	Ser	Ser	His	Glu	Ser	Ser	His	Gly	Thr
	130					135					140				
Pro	Ser	Gln	Thr	Thr	Ala	Lys	Asn	Trp	Glu	Leu	Thr	Ala	Ser	Ala	Ser
145					150					155					160

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
0	0.0000	0.0001	0.0002	0.0003	0.0004	0.0005	0.0006	0.0007	0.0008	0.0009	0.0010	0.0011	0.0012	0.0013	0.0014	0.0015	0.0016	0.0017	0.0018	0.0019	0.0020	0.0021	0.0022	0.0023	0.0024	0.0025	0.0026	0.0027	0.0028	0.0029	0.0030	0.0031	0.0032	0.0033	0.0034	0.0035	0.0036	0.0037	0.0038	0.0039	0.0040	0.0041	0.0042	0.0043	0.0044	0.0045	0.0046	0.0047	0.0048	0.0049	0.0050	0.0051	0.0052	0.0053	0.0054	0.0055	0.0056	0.0057	0.0058	0.0059	0.0060	0.0061	0.0062	0.0063	0.0064	0.0065	0.0066	0.0067	0.0068	0.0069	0.0070	0.0071	0.0072	0.0073	0.0074	0.0075	0.0076	0.0077	0.0078	0.0079	0.0080	0.0081	0.0082	0.0083	0.0084	0.0085	0.0086	0.0087	0.0088	0.0089	0.0090	0.0091	0.0092	0.0093	0.0094	0.0095	0.0096	0.0097	0.0098	0.0099	0.0100